

GenCore version 5.1.6

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OM protein - nucleic search, using frame_plus_p2n model

[illegible]

```
Title:          US-10-057-275-4
Perfect score:  703
Sequence:       1 MAQSLALSLLILVLAFGIPR.....KGKSGKCKRTERSQTPKGP 134
```

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop   6.0 , Delext  7.0
```

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 500 summaries
```

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlh
```

```
Q=/cgn2_1/USPTO_spool/US10057275/runat_03102003_131200_916/app_query.fasta_1.327
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=200 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10057275_@CGN_1_1_3508_@runat_03102003_131200_916 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : GenEmbl:*
identical search repeated in GENSEQ, USPATS, USPPUBS, and EST databases

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OM nucleic - nucleic search, using sw model

```
Run on:      October  4, 2003, 09:15:28 ; Search time 1945 Seconds
              (without alignments)
              8455.357 Million cell updates/sec
```

```
Title:          US-10-057-275-3
Perfect score:  402
Sequence:       1 ATGGCTCAGTCACTGGCTCT.....CACAGACCCCTAAAGGGCCA 402
```

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 60

Total number of hits satisfying chosen parameters: 33

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
identical search repeated in GENSEQ, USPATS, USPPUBS, and EST databases

OM nucleic - nucleic search, using sw model

Database : GenEmbl:*
identical search repeated in GENSEQ, USPATS, USPGPUBS, and EST databases